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RAW SEQUENCE LISTING

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Application Serial Number: 10/521, 584
Source: PCT
Date Processed by STIC: 10/25/2005

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/521,584

DATE: 10/25/2005
TIME: 13:39:55

Input Set : A:\BAS10029.app
Output Set: N:\CRF4\10252005\J521584.raw

4 <110> APPLICANT: REINDL, ANDREAS
6 <120> TITLE OF INVENTION: NADH-DEPEDENT CYTOCHROME b5 REDUCTASE AS TARGET FOR
HERBICIDES
8 <130> FILE REFERENCE: BASF.10029
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/521,584
C--> 11 <141> CURRENT FILING DATE: 2005-01-18
13 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07590
14 <151> PRIOR FILING DATE: 2003-07-14
16 <150> PRIOR APPLICATION NUMBER: DE 102 32 778
17 <151> PRIOR FILING DATE: 2002-07-18
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 846
25 <212> TYPE: DNA
26 <213> ORGANISM: Arabidopsis thaliana
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(843)
32 <400> SEQUENCE: 1
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34 Met Asp Thr Glu Phe Leu Arg Thr Leu Asp Arg Gln Ile Leu Leu Gly
35 1 5 10 15
37 gtc ttc gtt gct ttc gtc gcc gtt ggt gct ggt gct gct tat ttt ctt 96
38 Val Phe Val Ala Phe Val Ala Val Gly Ala Gly Ala Ala Tyr Phe Leu
39 20 25 30
41 aca tcc tcc aag aaa cgc aga gtg tgt ttg gat cca gag aat ttc aag 144
42 Thr Ser Ser Lys Lys Arg Arg Val Cys Leu Asp Pro Glu Asn Phe Lys
43 35 40 45
45 gag ttc aag ctt gtt aag aga cat cag ctt agt cac aat gtg gcc aag 192
46 Glu Phe Lys Leu Val Lys Arg His Gln Leu Ser His Asn Val Ala Lys
47 50 55 60
49 ttc gtt ttt gaa ctc cca act tct act tct gtg ttg ggt ctt ccc att 240
50 Phe Val Phe Glu Leu Pro Thr Ser Thr Ser Val Leu Gly Leu Pro Ile
51 65 70 75 80
53 gga caa cac atc agt tgc agg gga aag gat ggt caa gga gag gat gtt 288
54 Gly Gln His Ile Ser Cys Arg Gly Lys Asp Gly Gln Gly Glu Asp Val
55 85 90 95
57 att aag cca tac acc ccg act acg tta gac tct gac gtt gga cgt ttc 336
58 Ile Lys Pro Tyr Thr Pro Thr Thr Leu Asp Ser Asp Val Gly Arg Phe
59 100 105 110
61 gaa ctt gtc att aag atg tat ccg caa gga cgg atg tct cat cat ttc 384
62 Glu Leu Val Ile Lys Met Tyr Pro Gln Gly Arg Met Ser His His Phe
63 115 120 125

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65	agg gag atg cgt gtt gga gac cat ctt gcc gta aag gga cca aag ggt	432
66	Arg Glu Met Arg Val Gly Asp His Leu Ala Val Lys Gly Pro Lys Gly	
67	130 135 140	
69	agg ttc aag tat caa cca ggt cag ttt agg gca ttt gga atg ctt gct	480
70	Arg Phe Lys Tyr Gln Pro Gly Gln Phe Arg Ala Phe Gly Met Leu Ala	
71	145 150 155 160	
73	gga ggt tca ggc atc act ccc atg ttc caa gtg gcc aga gca att cta	528
74	Gly Gly Ser Gly Ile Thr Pro Met Phe Gln Val Ala Arg Ala Ile Leu	
75	165 170 175	
77	gaa aac cca aca gac aag aca aag gtg cat ctc att tac gcc aac gtc	576
78	Glu Asn Pro Thr Asp Lys Thr Lys Val His Leu Ile Tyr Ala Asn Val	
79	180 185 190	
81	aca tac gac gac att ctc ttg aag gaa ttg gag ggt ctt act acc	624
82	Thr Tyr Asp Asp Ile Leu Leu Lys Glu Glu Leu Glu Gly Leu Thr Thr	
83	195 200 205	
85	aat tac cct gaa caa ttt aaa atc ttc tat gtt ttg aac cag cct ccg	672
86	Asn Tyr Pro Glu Gln Phe Lys Ile Phe Tyr Val Leu Asn Gln Pro Pro	
87	210 215 220	
89	gaa gta tgg gat ggt gtt gga ttt gta tca aag gaa atg att cag	720
90	Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln	
91	225 230 235 240	
93	act cat tgc cct gca cct gca tct gat att cag atc cta aga tgc gga	768
94	Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly	
95	245 250 255	
97	cca ccg cca atg aac aag gcc atg gct gca aac ctt gaa gct ctg gga	816
98	Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly	
99	260 265 270	
101	tac tct ccg gag atg caa ttc cag ttc tga	846
102	Tyr Ser Pro Glu Met Gln Phe Gln Phe	
103	275 280	
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108	<212> TYPE: PRT	
109	<213> ORGANISM: Arabidopsis thaliana	
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116	20 25 30	
118	Thr Ser Ser Lys Lys Arg Arg Val Cys Leu Asp Pro Glu Asn Phe Lys	
119	35 40 45	
121	Glu Phe Lys Leu Val Lys Arg His Gln Leu Ser His Asn Val Ala Lys	
122	50 55 60	
124	Phe Val Phe Glu Leu Pro Thr Ser Thr Ser Val Leu Gly Leu Pro Ile	
125	65 70 75 80	
127	Gly Gln His Ile Ser Cys Arg Gly Lys Asp Gly Gln Gly Glu Asp Val	
128	85 90 95	
130	Ile Lys Pro Tyr Thr Pro Thr Leu Asp Ser Asp Val Gly Arg Phe	
131	100 105 110	

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133 Glu Leu Val Ile Lys Met Tyr Pro Gln Gly Arg Met Ser His His Phe
134 115 120 125
136 Arg Glu Met Arg Val Gly Asp His Leu Ala Val Lys Gly Pro Lys Gly
137 130 135 140
139 Arg Phe Lys Tyr Gln Pro Gly Gln Phe Arg Ala Phe Gly Met Leu Ala
140 145 150 155 160
142 Gly Gly Ser Gly Ile Thr Pro Met Phe Gln Val Ala Arg Ala Ile Leu
143 165 170 175
145 Glu Asn Pro Thr Asp Lys Thr Lys Val His Leu Ile Tyr Ala Asn Val
146 180 185 190
148 Thr Tyr Asp Asp Ile Leu Leu Lys Glu Glu Leu Glu Gly Leu Thr Thr
149 195 200 205
151 Asn Tyr Pro Glu Gln Phe Lys Ile Phe Tyr Val Leu Asn Gln Pro Pro
152 210 215 220
154 Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln
155 225 230 235 240
157 Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly
158 245 250 255
160 Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly
161 260 265 270
163 Tyr Ser Pro Glu Met Gln Phe Gln Phe
164 275 280
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168 <211> LENGTH: 729
169 <212> TYPE: DNA
170 <213> ORGANISM: Nicotiana tabacum
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (1)..(726)
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178 Val Cys Leu Asp Pro Glu Arg Phe Lys Glu Phe Lys Leu Val Lys Arg
179 1 5 10 15
181 aca caa ata agc cac aat gtt gca aag ttc aga ttt gaa ctc ccc aca 96
182 Thr Gln Ile Ser His Asn Val Ala Lys Phe Arg Phe Glu Leu Pro Thr
183 20 25 30
185 cct act tct gta ttg ggc cta ccc att gga caa cat att agt tgc agg 144
186 Pro Thr Ser Val Leu Gly Leu Pro Ile Gly Gln His Ile Ser Cys Arg
187 35 40 45
189 ggc aag gat agt caa ggt gaa gag gtt gtt aaa ccg tac aca cca act 192
190 Gly Lys Asp Ser Gln Gly Glu Glu Val Val Lys Pro Tyr Thr Pro Thr
191 50 55 60
193 act ttg gat tca gat gtt gga tat ttt gaa cta gtt att aag atg tat 240
194 Thr Leu Asp Ser Asp Val Gly Tyr Phe Glu Leu Val Ile Lys Met Tyr
195 65 70 75 80
197 cct caa gga agg atg tct cat cat ttc cga gaa atg cgt gag ggt gat 288
198 Pro Gln Gly Arg Met Ser His His Phe Arg Glu Met Arg Glu Gly Asp
199 85 90 95
201 tat ttg gct gtg aag gga cct aag ggc cgc ttt aag tac cag cct ggc 336

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202	Tyr	Leu	Ala	Val	Lys	Gly	Pro	Lys	Gly	Arg	Phe	Lys	Tyr	Gln	Pro	Gly	
203	100							105						110			
205	caa	gtg	aga	gca	ttt	gga	atg	ctt	gct	gga	ggc	tct	ggc	att	acc	cca	384
206	Gln	Val	Arg	Ala	Phe	Gly	Met	Leu	Ala	Gly	Gly	Ser	Gly	Ile	Thr	Pro	
207	115							120						125			
209	atg	ttt	cag	gtt	gct	aga	gct	att	ctc	gaa	aat	cca	aat	gac	aag	aca	432
210	Met	Phe	Gln	Val	Ala	Arg	Ala	Ile	Leu	Glu	Asn	Pro	Asn	Asp	Lys	Thr	
211	130							135						140			
213	aag	gtg	cac	ttg	ata	tat	gct	aat	gtt	acc	tat	gaa	gac	ata	ctt	tta	480
214	Lys	Val	His	Leu	Ile	Tyr	Ala	Asn	Val	Thr	Tyr	Glu	Asp	Ile	Leu	Leu	
215	145							150				155			160		
217	aag	gaa	cag	ttg	gat	ggc	ctt	gct	gct	aac	tat	cct	gac	cgt	ttc	aaa	528
218	Lys	Glu	Gln	Leu	Asp	Gly	Leu	Ala	Ala	Asn	Tyr	Pro	Asp	Arg	Phe	Lys	
219								165				170			175		
221	att	tat	tac	gtt	ctg	aat	cag	cct	cct	gaa	gta	tgg	agc	ggt	ggt	gtt	576
222	Ile	Tyr	Tyr	Val	Leu	Asn	Gln	Pro	Pro	Glu	Val	Trp	Ser	Gly	Gly	Val	
223								180			185			190			
225	gga	ttt	gtg	tcc	aag	gaa	atg	att	cag	act	cat	tgt	cct	gcc	ccg	gca	624
226	Gly	Phe	Val	Ser	Lys	Glu	Met	Ile	Gln	Thr	His	Cys	Pro	Ala	Pro	Ala	
227								195			200			205			
229	tct	gac	att	cag	ata	ctg	agg	tgt	ggt	cca	cct	cca	atg	aac	aag	gct	672
230	Ser	Asp	Ile	Gln	Ile	Leu	Arg	Cys	Gly	Pro	Pro	Pro	Met	Asn	Lys	Ala	
231								210			215			220			
233	atg	gct	gct	cat	ctt	gaa	gcc	ctt	gga	tac	acc	cca	gag	atg	caa	ttc	720
234	Met	Ala	Ala	His	Leu	Glu	Ala	Leu	Gly	Tyr	Thr	Pro	Glu	Met	Gln	Phe	
235	225							230				235			240		
237	cag	ttt	taa													729	
238	Gln	Phe															
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244	<212>	TYPE:	PRT														
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249	1				5				10					15			
251	Thr	Gln	Ile	Ser	His	Asn	Val	Ala	Lys	Phe	Arg	Phe	Glu	Leu	Pro	Thr	
252								20			25			30			
254	Pro	Thr	Ser	Val	Leu	Gly	Leu	Pro	Ile	Gly	Gln	His	Ile	Ser	Cys	Arg	
255								35			40			45			
257	Gly	Lys	Asp	Ser	Gln	Gly	Glu	Glu	Val	Val	Lys	Pro	Tyr	Thr	Pro	Thr	
258								50			55			60			
260	Thr	Leu	Asp	Ser	Asp	Val	Gly	Tyr	Phe	Glu	Leu	Val	Ile	Lys	Met	Tyr	
261		65				70				75				80			
263	Pro	Gln	Gly	Arg	Met	Ser	His	His	Phe	Arg	Glu	Met	Arg	Glu	Gly	Asp	
264						85				90				95			
266	Tyr	Leu	Ala	Val	Lys	Gly	Pro	Lys	Gly	Arg	Phe	Lys	Tyr	Gln	Pro	Gly	
267						100				105				110			
269	Gln	Val	Arg	Ala	Phe	Gly	Met	Leu	Ala	Gly	Gly	Ser	Gly	Ile	Thr	Pro	
270						115				120				125			

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272 Met Phe Gln Val Ala Arg Ala Ile Leu Glu Asn Pro Asn Asp Lys Thr
273 130 135 140
275 Lys Val His Leu Ile Tyr Ala Asn Val Thr Tyr Glu Asp Ile Leu Leu
276 145 150 155 160
278 Lys Glu Gln Leu Asp Gly Leu Ala Ala Asn Tyr Pro Asp Arg Phe Lys
279 165 170 175
281 Ile Tyr Tyr Val Leu Asn Gln Pro Pro Glu Val Trp Ser Gly Gly Val
282 180 185 190
284 Gly Phe Val Ser Lys Glu Met Ile Gln Thr His Cys Pro Ala Pro Ala
285 195 200 205
287 Ser Asp Ile Gln Ile Leu Arg Cys Gly Pro Pro Pro Met Asn Lys Ala
288 210 215 220
290 Met Ala Ala His Leu Glu Ala Leu Gly Tyr Thr Pro Glu Met Gln Phe
291 225 230 235 240
293 Gln Phe
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298 <211> LENGTH: 32
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Primer
305 <400> SEQUENCE: 5
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309 <210> SEQ ID NO: 6
310 <211> LENGTH: 32
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Primer
317 <400> SEQUENCE: 6
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321 <210> SEQ ID NO: 7
322 <211> LENGTH: 20
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Primer
329 <400> SEQUENCE: 7
330 gctatgacca tgattacgcc 20
333 <210> SEQ ID NO: 8
334 <211> LENGTH: 18
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence
338 <220> FEATURE:
339 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic Primer
341 <400> SEQUENCE: 8
342 tgagacatcc gtccttgc 18
345 <210> SEQ ID NO: 9
346 <211> LENGTH: 20

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/521,584

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Input Set : A:\BAS10029.app

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date